RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/574.639
Source:	15WO.
Date Processed by STIC:	3/2/07

ENTERED



IFWO

RAW SEQUENCE LISTINGPATENT APPLICATION: **US/10/574,639**DATE: 03/02/2007

TIME: 12:58:04

Input Set : N:\efs\03 02 07\10574639 efs\seqlisting.txt

```
3 <110> APPLICANT: Thiry, Michel
            Dheur, Ingrid
      6 <120> TITLE OF INVENTION: Piscirickettsia Salmonis Antigens and Use Thereof
      8 <130> FILE REFERENCE: 425.1018
     10 <140> CURRENT APPLICATION NUMBER: 10/574,639
C--> 11 <141> CURRENT FILING DATE: 2006-03-31
     13 <150> PRIOR APPLICATION NUMBER: PCT/IB2004/03339
     14 <151> PRIOR FILING DATE: 2004-10-01
     16 <150> PRIOR APPLICATION NUMBER: 2003/0743
     17 <151> PRIOR FILING DATE: 2003-10-07
     19 <160> NUMBER OF SEQ ID NOS: 19
     21 <170> SOFTWARE: PatentIn version 3.3
     23 <210> SEQ ID NO: 1
     24 <211> LENGTH: 1314
     25 <212> TYPE: DNA
     26 <213> ORGANISM: Piscirickettsia salmonis
     29 <220> FEATURE:
     30 <221> NAME/KEY: CDS
     31 <222> LOCATION: (1)..(1314)
     33 <400> SEQUENCE: 1
     34 atg aaa gta aaa atg att gtt gca gct gta gct gtt gca ggt tta aca
                                                                               48
     35 Met Lys Val Lys Met Ile Val Ala Ala Val Ala Gly Leu Thr
                                            10
     38 qcq act qcc qca aat qcc gct gat aat ggt aag ctt caa tta caa atc
                                                                               96
     39 Ala Thr Ala Ala Asn Ala Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile
     40
                    20
                                        25
     42 aac caa ttg aag gcg caa cac act caa ctt caa cag caa gtt gct aat
                                                                              144
     43 Asn Gln Leu Lys Ala Gln His Thr Gln Leu Gln Gln Val Ala Asn
                                    40
                                                                              192
     46 ctg caa ggt caa ggc caa act act ggt gcc gtt cac gtt ggc gct gtt
     47 Leu Gln Gly Gln Gly Gln Thr Thr Gly Ala Val His Val Gly Ala Val
                                55
     50 ggt ggt gaa cta atc tct gaa aat aac tac gat ggt cgt ggc tta gat
                                                                              240
     51 Gly Gly Glu Leu Ile Ser Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp
                            70
     54 ctt ctt aaa tca tta gcg aaa gca ggc agc aat gca ccg tta tta act
                                                                              288
     55 Leu Leu Lys Ser Leu Ala Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr
                                                                              336
     58 att ggt ggt acg tta gaa gct gat gcg caa atg aac cgt aac ggt aat
     59 Ile Gly Gly Thr Leu Glu Ala Asp Ala Gln Met Asn Arg Asn Gly Asn
     60
                    100
     62 gtt gga tet ggt tet aet tet ggt gae eet tet gge ett aac tat aet
                                                                              384
     63 Val Gly Ser Gly Ser Thr Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr
```

RAW SEQUENCE LISTING DATE: 03/02/2007 PATENT APPLICATION: US/10/574,639 TIME: 12:58:04

Input Set : N:\efs\03 02 07\10574639 efs\seqlisting.txt

64 115		120	125
	age agt tet gea		act gca cgt att gat 432
			Thr Ala Arg Ile Asp
68 130	135	The Tyr Lea hop	140
		tag att aac aat	gaa atc tcg tat gac 480
			Glu Ile Ser Tyr Asp
72 145	15.0	11p var Asii Gry	160
			ctt tta gtg ggt aac 528
			Leu Leu Val Gly Asn
-		170	175
76	165		
			5
	=		Lys Phe Tyr Pro Asp 190
= =	180	185	
_	Phe Giu Leu Ala	=	Tyr Ser Ser Leu
84 195		200	205 ggt gga tet gta gge 672
			33 3 3 .
		Asp Ala Gin Asn	Gly Ala Ser Val Gly
88 210 ,	215		220
			gca ttt aaa acg tct 720
	_		Ala Phe Lys Thr Ser
92 225	230	235	240
			gca act agt gat tgg 768
			Ala Thr Ser Asp Trp
96	245	250	255
			caa gtc aat gcc act 816
			Gln Val Asn Ala Thr
100	260	265	270
			t acc aat gac agc ttc 864
-			n Thr Asn Asp Ser Phe
104 275		280	285
			a gat cgg cta ccg atg 912
			s Asp Arg Leu Pro Met
108 290	29		300
			a ttt gaa gcc ctt gct 960
			o Phe Glu Ala Leu Ala
112 305	310	31	
			t act aca ggt ggt aca 1008
-	-	_	n Thr Thr Gly Gly Thr
116	325	330	335
			t tac cac ttc caa gct 1056
-			a Tyr His Phe Gln Ala
120	340	345	350
			c cgt aca tat ggc ttt 1104
_			r Arg Thr Tyr Gly Phe
124 355		360	365
	gga cct gtt ga	t cag ttt att ga	t ggt aat act gcg att 1152
127 Asp Lys Val 128 370		Gln Phe Ile As	p Gly Asn Thr Ala Ile 380

RAW SEQUENCE LISTING DATE: 03/02/2007 PATENT APPLICATION: US/10/574,639 TIME: 12:58:04

Input Set : N:\efs\03_02_07\10574639_efs\seqlisting.txt

							-				_	ggt	_				1200
	385	ire	ASII	ASII	гуѕ	ъуs 390	Asp	GIII	пр	Leu	395	Gly	vai	ASII	ser	400	
		ttt	aag	aac	aca		gtt	ggt	ctt	gag	tat	gcg	cgt	gta	ggt	cag	1248
135	Val	Phe	Lys	Asn	Thr	Thr	Val	${\tt Gly}$	Leu	Glu	Tyr	Ala	Arg	Val		Gln	
136					405					410					415		1006
												aac					1296
140	Leu	Asp	ser	420	GIY	Thr	Asp	THE	425	Arg	Tyr	Asn	vai	430	TIIL	Ата	
	gat	ato	act		aag	ttc			423					430			1314
	-	-			Lys												
144			435														
147	<210	O> SI	EQ II	NO:	: 2												
.148	<210> SEQ ID NO: 2 <211> LENGTH: 438																
149	19 <212> TYPE: PRT																
150	<21.	3 > OI	RGAN	ISM:	Pisc	cirio	ckett	sia	salı	nonis	3						
	<400					_	_	_	_						_		
		Lys	Val	Lys		Ile	Val	Ala	Ala		Ala	Val	Ala	GLY		Thr	
155		CT1		77-	5	7.7 -	37 -	7	3	10	T	т	~1 ·-	T	15	т1 -	
	Ala	Thr	Ala		Asn	Ата	Ата	Asp	Asn 25	GIY	ьys	Leu	GIN	ьеu 30	GIII	ıте	
159	λαn	Gl n	T.011	20 Tage	71 a	Gln	Hic	Thr		T. - 11	Gl n	Gln	Gln		Δla	Δsn	
163	Poli	GIII	35	цуз	AIG	GIII	1112	40	GIII	пси	0111	GIII	45	vai	nia	11011	
	Leu	Gln		Gln	Glv	Gln	Thr		Glv	Ala	Val	His		Gly	Ala	Val	
167		50			2		55					60		•			
170	Gly	Gly	Glu	Leu	Ile	Ser	Glu	Asn	Asn	Tyr	Asp	Gly	Arg	Gly	Leu	Asp	
171						70					75					80	
	Leu	Leu	Lys	Ser		Ala	Lys	Ala	Gly		Asn	Ala	Pro	Leu		Thr	
175		- -			85			_		90		_	_	_	95	_	
	Ile	GLY	GIY		Leu	Glu	Ala	Asp		GIn	Met	Asn	Arg		GLY	Asn	
179	37-1	C111	cor	100	602	Thr	802	Clv.	105	Dro	cor	Gly	T.011	110	Туг	Thr	
183	vai	GIY	115	Gry	Ser	1111	Ser	120	АЗР	110	Der	Gry	125	ASII	- 7 -	1111	
	Asp	Glv		Ser	Ser	Ser	Ala		Tyr	Leu	Asp	Thr		Arq	Ile	Asp	
187	-	130					135		•		-	140		_		-	
190	Ile	Leu	Ala	His	Val	Asn	Asp	Trp	Val	Asn	Gly	Glu	Ile	Ser	Tyr	Asp	
	145					150					155					160	
194	Leu	Asn	Gly	Asp	Ser	Gly	Leu	His	Thr	Gly	Ser	Leu	Leu	Val	Gly	Asn	
195			_		165	_		_		170	_				175	_	
	Leu	Asn	Gln		Pro	Val	Tyr	Gly		Ile	Gly	Lys	Phe		Pro	Asp	
199		6 1	T	180	~1	T	77.	0	185	7	77-7	m	0	190	0	T 011	
	АТа	GTĀ		rne	GIU	ьeu	Ala	200	Asp	Asp	٧aı	Tyr	205	ser	ser	ьeu	
203	V-1	Lare	195	Тъг	Dha	Δτα	Dro		בוג	Gln	λen	Gly		Ser	Val	Glv	
207	vaı	210	nr 9	- y -	1116	nr 9	215	roh	TIG	CIII	HOII	220	лта	Der	V 4.1	~~y	
	Phe		Lvs	Ala	Glv	Leu		Thr	Ser	Leu	Thr	Ala	Phe	Lvs	Thr	Ser	
	225	- , -	_1 -		2	230					235			4		240	
		Pro	Gln	Ala	Asn		Ala	Asn	Tyr	Asn		Ala	Thr	Ser	Asp	Trp	
215					245				-	.250					255		
•																	

RAW SEQUENCE LISTING DATE: 03/02/2007 PATENT APPLICATION: US/10/574,639 TIME: 12:58:04

Input Set : N:\efs\03_02_07\10574639_efs\seqlisting.txt

	Ser	Ala	Gln		Asp	Tyr	Thr	Phe	Asn 265	Ala	Gly	Gln	Val	Asn 270	Ala	Thr	
219	-1-	~ 1	77-	260		+	G	7		77- T	7	mb	7		C - ~	Dho	
	TTE	GIY		GIY	Tyr	ьeu	ser		Mec	Val	ASII	IIII		Asp	ser	FIIE	
223			275	~ 3		~ 1	m)	280	m1	~ 1	T	7	285	T	D	Mat	
	Thr		Thr	GIÀ	Ala	GIA		GIY	Thr	GIN	гÀг		Arg	ьeu	PIO	Met	
227		290		_		_	295	~7	-1	~1	5	300	~3		.	21-	
		Asn	Val	ser	Ala	_	тте	GLY	Pne	GIY			GIU	Ala	Leu		
	305			~7	em1	310	_	~1	.		315		m1	a 1	~1	320	
	Thr	Tyr	Ala	GIn	Thr	Leu	Lys	Gly	Leu		Asn	Thr	Thr	GIA		Inr	
235		_	_	_	325		_	_		330		_		-1	335		
	Thr	Lys	Leu		Ala	Phe	Asp	Leu		GIY	Ата	ıyr	HIS		GIN	Ala	
239		_	_	340				_	345	_			-	350	~ 1	D1	
	Val	Lys		Met	Thr	Val	Met		GIY	Tyr	ser	Arg			GIA	Pne	
243	_	_	355		_		_	360	-1			~1	365	, ml	77-	T7 -	
	Asp	_	Val	GIY	Pro	Val		GIn	Phe	IIe	Asp		Asn	Thr	Ата	TIE	
247		370		_	_	_	375		_	_	_	380			~	~1	
		Ile	Asn	Asn	Lys	_	Asp	Gin	Trp	Leu		GIY	vai	Asn	ser		
	385		_	_		390	-		_		395		_	7	~7	400	
	Val	Phe	Lys	Asn	Thr	Thr	Val	GIY	Leu		Tyr	Ala	Arg	Val		GIn	
255	_	_	_		405		_		_	410	_	_		_	415		
		Asp	Ser		Gly	Thr	Asp	Thr		Arg	Tyr	Asn	Val		Thr	Ala	
259				420	_				425					430			
	Asp	Met		Val	Lys	Phe											
263			435														
					_												
				O NO													
267	<21	1> L	ENGTI	H: 12		,											
267 268	<213	1> Ll 2> T	ENGTI YPE:	H: 12 DNA	248	,		. •	- 7	•	_						
267 268 269	<213 <213 <213	1> L1 2> T3 3> O1	ENGTI YPE: RGAN:	H: 12 DNA ISM:		cirio	ckett	sia	salı	nonis	5						
267 268 269 272	<213 <213 <213 <220	1> L1 2> T3 3> O1 0> F1	ENGTI YPE: RGAN: EATUI	H: 12 DNA ISM: RE:	248 Pis	cirio	ckett	sia	salı	nonis	5		·				
267 268 269 272 273	<213 <213 <213 <220 <223	1> L1 2> T1 3> O1 0> F1 1> N2	ENGTI YPE: RGAN: EATUI AME/I	H: 12 DNA ISM: RE: KEY:	248 Piso CDS			sia	salı	nonis	3						
267 268 269 272 273 274	<21: <21: <21: <22: <22: <22:	1 > L1 2 > T 3 > O1 0 > F1 1 > N2 2 > L0	ENGTI YPE: RGAN: EATUI AME/I	H: 12 DNA ISM: RE: KEY: ION:	248 Piso CDS (1)			csia	salı	nonis	5		·				÷
267 268 269 272 273 274 276	<213 <213 <213 <223 <223 <223 <400	1 > L1 2 > T1 3 > O1 0 > F1 1 > N2 2 > L0 0 > S1	ENGTI YPE: RGANI EATUI AME/I OCATI	H: 12 DNA ISM: RE: KEY: ION:	248 Piso CDS (1) 3	(1	248)								~~~	422	
267 268 269 272 273 274 276 277	<21: <21: <22: <22: <22: <40: gct	1 > L1 2 > T 3 > O1 0 > F1 1 > N2 2 > L0 0 > S1 gat	ENGTI YPE: RGAN: EATUI AME/I OCAT: EQUEI aat	H: 12 DNA ISM: RE: KEY: ION: NCE:	Piso CDS (1) 3 aag	(1:	248) caa	tta	caa	atc	aac						. 48
267 268 269 272 273 274 276 277	<21: <21: <22: <22: <22: <40: gct Ala	1 > L1 2 > T 3 > O1 0 > F1 1 > N2 2 > L0 0 > S1 gat	ENGTI YPE: RGAN: EATUI AME/I OCAT: EQUEI aat	H: 12 DNA ISM: RE: KEY: ION: NCE: ggt	Piso CDS (1) 3 aag Lys	(1:	248) caa	tta	caa	atc Ile	aac				Ala		. 48
267 268 269 272 273 274 276 277 278 279	<21: <21: <22: <22: <22: <40: gct Ala 1	1 > L1 2 > T3 3 > O1 0 > F1 1 > N2 2 > L0 0 > S1 gat Asp	ENGTH YPE: RGAN: EATUH AME/I OCAT: EQUEN aat Asn	H: 12 DNA ISM: RE: KEY: ION: NCE: ggt Gly	Piso CDS (1) 3 aag Lys 5	(12 ctt Leu	248) caa Gln	tta Leu	caa Gln	atc Ile 10	aac Asn	Gln	Leu	Lys	Ala 15	Gln	
267 268 269 272 273 274 276 277 278 279 281	<21: <21: <22: <22: <22: <40: gct Ala 1	1 > L1 2 > T 3 > O1 0 > F1 1 > N 2 > L 0 > S1 gat Asp	ENGTI YPE: RGANI EATUI AME/I DCATI EQUEI aat Asn	H: 12 DNA ISM: RE: KEY: ION: GE: GGly ctt	Piso CDS (1) 3 aag Lys 5 caa	(12 ctt Leu cag	248) caa Gln caa	tta Leu gtt	caa Gln gct	atc Ile 10 aat	aac Asn ctg	Gln caa	Leu ggt	Lys caa	Ala 15 ggc	Gln caa	48 96
267 268 269 272 273 274 276 277 278 279 281 282	<21: <21: <22: <22: <22: <40: gct Ala 1	1 > L1 2 > T 3 > O1 0 > F1 1 > N 2 > L 0 > S1 gat Asp	ENGTI YPE: RGANI EATUI AME/I DCATI EQUEI aat Asn	H: 12 DNA ISM: RE: REY: ION: GOY Gly ctt Leu	Piso CDS (1) 3 aag Lys 5	(12 ctt Leu cag	248) caa Gln caa	tta Leu gtt	caa Gln gct Ala	atc Ile 10 aat	aac Asn ctg	Gln caa	Leu ggt	Lys caa Gln	Ala 15 ggc	Gln caa	
267 268 269 272 273 274 276 277 278 279 281 282 283	<21: <21: <22: <22: <40: gct Ala 1 cac	1 > L1 2 > T 3 > O1 0 > F1 1 > N2 2 > L0 0 > S1 gat Asp act Thr	ENGTH YPE: RGAN: EATUH AME/I DCAT: DCAT: EQUEN aat Asn caa Gln	H: 12 DNA ISM: RE: RE: ION: GE: GGly ctt Leu 20	Piso CDS (1) 3 aag Lys 5 caa Gln	ctt Leu cag	caa Gln caa Gln	tta Leu gtt Val	caa Gln gct Ala 25	atc Ile 10 aat Asn	aac Asn ctg Leu	Gln caa Gln	Leu ggt Gly	Lys caa Gln 30	Ala 15 ggc Gly	Gln caa Gln	96
267 268 269 272 273 274 276 277 278 279 281 282 283 285	<21: <21: <22: <22: <40: gct Ala 1 cac His	1 > L1 2 > T 3 > O1 0 > F1 1 > N2 2 > L0 0 > S1 gat Asp act Thr	ENGTH YPE: RGAN: EATUH AME/I CCAT: EQUEN aat Asn caa Gln	H: 12 DNA ISM: RE: RE: ION: RE: GOT Gly ctt Leu 20 gcc	Piso CDS (1) 3 aag Lys 5 caa Gln	ctt Leu cag Gln	caa Gln caa Gln gtt	tta Leu gtt Val	caa Gln gct Ala 25 gct	atc Ile 10 aat Asn gtt	aac Asn ctg Leu	Gln caa Gln ggt	Leu ggt Gly gaa	Lys caa Gln 30 cta	Ala 15 ggc Gly atc	Gln caa Gln tct	
267 268 269 272 273 274 276 277 281 282 283 285 286	<21: <21: <22: <22: <40: gct Ala 1 cac His	1 > L1 2 > T 3 > O1 0 > F1 1 > N2 2 > L0 0 > S1 gat Asp act Thr	ENGTH YPE: RGANI EATUH AME/I OCATI OCATI EQUEN aat Asn caa Gln ggt Gly	H: 12 DNA ISM: RE: RE: ION: RE: GOT Gly ctt Leu 20 gcc	Piso CDS (1) 3 aag Lys 5 caa Gln	ctt Leu cag Gln	caa Gln caa Gln gtt	tta Leu gtt Val ggc Gly	caa Gln gct Ala 25 gct	atc Ile 10 aat Asn gtt	aac Asn ctg Leu	Gln caa Gln ggt	Leu ggt Gly gaa Glu	Lys caa Gln 30 cta	Ala 15 ggc Gly atc	Gln caa Gln tct	96
267 268 269 272 273 274 276 277 281 282 283 285 286 287	<21: <21: <22: <22: <22: <40: gct Ala 1 cac His act Thr	1 > L1 2 > T' 3 > O1 0 > F1 1 > N2 2 > L0 0 > S1 gat Asp act Thr act	ENGTH YPE: RGANT EATUR AME/I OCATT OCATT EQUEN ASD Caa Gln ggt Gly 35	H: 12 DNA ISM: RE: REY: ION: GGly ctt Leu 20 gcc Ala	Piso CDS (1) 3 aag Lys 5 caa Gln gtt Val	ctt Leu cag Gln cac	caa Gln caa Gln gtt Val	tta Leu gtt Val ggc Gly 40	caa Gln gct Ala 25 gct Ala	atc Ile 10 aat Asn gtt Val	aac Asn ctg Leu ggt Gly	Gln caa Gln ggt Gly	ggt Gly gaa Glu 45	Lys caa Gln 30 cta Leu	Ala 15 ggc Gly atc Ile	caa Gln tct Ser	96 144
267 268 269 272 273 274 276 277 281 282 283 285 286 287 289	<21: <21: <22: <22: <22: <40: gct Ala 1 cac His act Thr	1 > LI 2 > T' 3 > OI 0 > FI 1 > NZ 2 > LO 0 > SI gat Asp act Thr act Thr	ENGTH YPE: RGANT EATUR AME/I OCATT OCATT EQUER ASD CAA Gln Ggt Gly 35 aac	H: 12 DNA ISM: RE: REY: ION: GGly ctt Leu 20 gcc Ala tac	Piso CDS (1) 3 aag Lys 5 caa Gln gtt Val	ctt Leu cag Gln cac His	caa Gln caa Gln gtt Val	tta Leu gtt Val ggc Gly 40 ggc	caa Gln gct Ala 25 gct Ala tta	atc Ile 10 aat Asn gtt Val	aac Asn ctg Leu ggt Gly	Gln caa Gln ggt Gly	ggt Gly gaa Glu 45 aaa	caa Gln 30 cta Leu	Ala 15 ggc Gly atc Ile	caa Gln tct ser	96
267 268 269 272 273 274 276 277 278 279 281 282 283 285 286 287 289	<21: <21: <22: <22: <22: <40: gct Ala 1 cac His act Thr	1 > LI 2 > T 3 > OI 0 > FI 1 > NI 2 > LO 0 > SI gat Asp act Thr act Thr aat Asn	ENGTH YPE: RGANT EATUR AME/I OCATT OCATT EQUER ASD CAA Gln Ggt Gly 35 aac	H: 12 DNA ISM: RE: REY: ION: GGly ctt Leu 20 gcc Ala tac	Piso CDS (1) 3 aag Lys 5 caa Gln gtt Val	ctt Leu cag Gln cac His	caa Gln caa Gln gtt Val cgt Arg	tta Leu gtt Val ggc Gly 40 ggc	caa Gln gct Ala 25 gct Ala tta	atc Ile 10 aat Asn gtt Val	aac Asn ctg Leu ggt Gly	caa Gln ggt Gly ctt Leu	ggt Gly gaa Glu 45 aaa	caa Gln 30 cta Leu	Ala 15 ggc Gly atc Ile	caa Gln tct ser	96 144
267 268 269 272 273 274 276 277 278 282 283 285 286 287 289 290	<21: <21: <22: <22: <22: <400 gct Ala 1 cac His act Thr gaa Glu	1 > LI 2 > T' 3 > OI 0 > FI 1 > NI 2 > LO 0 > SI gat Asp act Thr act Thr ast Asn 50	ENGTH YPE: RGANI REATUR AME/I OCATI EQUEN aat Asn caa Gln ggt Gly 35 aac Asn	H: 12 DNA ISM: RE: REY: ION: GOY Ctt Leu 20 gcc Ala tac Tyr	Piso CDS (1) 3 aag Lys 5 caa Gln gtt Val gat Asp	ctt Leu cag Gln cac His	caa Gln caa Gln gtt Val cgt Arg	tta Leu gtt Val ggc Gly 40 ggc Gly	caa Gln gct Ala 25 gct Ala tta Leu	atc Ile 10 aat Asn gtt Val gat Asp	aac Asn ctg Leu ggt Gly ctt Leu	caa Gln ggt Gly ctt Leu 60	ggt Gly gaa Glu 45 aaa Lys	caa Gln 30 cta Leu tca Ser	Ala 15 ggc Gly atc Ile tta Leu	Gln caa Gln tct Ser gcg Ala	96 144 192
267 268 269 272 273 274 276 277 278 281 282 283 285 286 287 289 290 291 293	<21: <21: <22: <22: <40: gct Ala 1 cac His act Thr gaa Glu aaa	1 > LI 2 > T 3 > OI 0 > FI 1 > NI 2 > LO 0 > SI gat Asp act Thr act Thr aat Asn 50 gca	ENGTH YPE: RGAN: RGAN: REQUENT AST CAA Gln Gly 35 AST AST Gly 35 AST AST	H: 12 DNA ISM: RE: REY: RON: GGly ctt Leu 20 gcc Ala tac Tyr agc	Piso CDS (1) 3 aag Lys 5 caa Gln gtt Val gat Asp	ctt Leu cag Gln cac His ggt Gly	caa Gln caa Gln gtt Val cgt Arg 55 ccg	tta Leu gtt Val ggc Gly 40 ggc Gly tta	caa Gln gct Ala 25 gct Ala tta Leu	atc Ile 10 aat Asn gtt Val gat Asp	aac Asn ctg Leu ggt Gly ctt Leu	caa Gln ggt Gly ctt Leu 60 ggt	ggt Gly gaa Glu 45 aaa Lys	caa Gln 30 cta Leu tca Ser	Ala 15 ggc Gly atc Ile tta Leu	Gln caa Gln tct Ser gcg Ala gaa	96 144
267 268 269 272 273 274 276 277 278 279 281 282 283 285 286 287 290 291 293 294	<21: <21: <22: <22: <40: gct Ala 1 cac His act Thr gaa Glu aaa Lys	1 > LI 2 > T 3 > OI 0 > FI 1 > NI 2 > LO 0 > SI gat Asp act Thr act Thr aat Asn 50 gca	ENGTH YPE: RGAN: RGAN: REQUENT AST CAA Gln Gly 35 AST AST Gly 35 AST AST	H: 12 DNA ISM: RE: REY: RON: GGly ctt Leu 20 gcc Ala tac Tyr agc	Piso CDS (1) 3 aag Lys 5 caa Gln gtt Val gat Asp	ctt Leu cag Gln cac His ggt Gly gca Ala	caa Gln caa Gln gtt Val cgt Arg 55 ccg	tta Leu gtt Val ggc Gly 40 ggc Gly tta	caa Gln gct Ala 25 gct Ala tta Leu	atc Ile 10 aat Asn gtt Val gat Asp	aac Asn ctg Leu ggt Gly ctt Leu att	caa Gln ggt Gly ctt Leu 60 ggt	ggt Gly gaa Glu 45 aaa Lys	caa Gln 30 cta Leu tca Ser	Ala 15 ggc Gly atc Ile tta Leu	caa Gln tct Ser gcg Ala gaa Glu	96 144 192
267 268 269 272 273 274 276 277 278 279 281 282 283 285 286 287 290 291 293 294 295	<21: <21: <22: <22: <40: gct Ala 1 cac His act Thr gaa Glu aaa Lys 65	1 > LI 2 > T 3 > OI 0 > FI 1 > NI 2 > LO 0 > SI gat Asp act Thr act Thr ast Asn 50 gca Ala	ENGTH YPE: RGAN: RGAN: EATUH AME/I OCAT: EQUEN aat Asn caa Gln ggt Gly 35 aac Asn	H: 12 DNA ISM: RE: REY: ROE: ROE: ROE: ROE	Piso CDS (1) 3 aag Lys 5 caa Gln gtt Val gat Asp	ctt Leu cag Gln cac His ggt Gly gca Ala 70	caa Gln caa Gln gtt Val cgt Arg 55 ccg Pro	tta Leu gtt Val ggc Gly 40 ggc Gly tta Leu	caa Gln gct Ala 25 gct Ala tta Leu tta	atc Ile 10 aat Asn gtt Val gat Asp act Thr	aac Asn ctg Leu ggt Gly ctt Leu att Ile 75	caa Gln ggt Gly ctt Leu 60 ggt Gly	ggt Gly gaa Glu 45 aaa Lys ggt Gly	Lys caa Gln 30 cta Leu tca Ser acg	Ala 15 ggc Gly atc Ile tta Leu	caa Gln tct Ser gcg Ala gaa Glu 80	96 144 192 240
267 268 269 272 273 274 276 277 278 279 281 282 283 285 287 290 291 293 294 295 297	<21: <21: <22: <22: <40: gct Ala 1 cac His act Thr gaa Glu aaa Lys gct	1 > LI 2 > T 3 > OI 0 > FI 1 > NI 2 > LO 0 > SI 0 > Gat Asp act Thr act Thr act Asn 50 gca Ala gat	ENGTH YPE: RGAN: RGAN: REQUEL ACT: EQUEL ACT: CAA Gln Gly 35 aac Acn Gly 35 acc Acn	H: 12 DNA: ISM: ISM: RE: ION:	Piso CDS (1) 3 aag Lys 5 caa Gln gtt Val gat Asp	ctt Leu cag Gln cac His ggt Gly gca Ala 70	caa Gln caa Gln gtt Val cgt Arg 55 ccg Pro	tta Leu gtt Val ggc Gly 40 ggc Gly tta Leu	caa Gln gct Ala 25 gct Ala tta Leu tta Leu	atc Ile 10 aat Asn gtt Val gat Asp act Thr	aac Asn ctg Leu ggt Gly ctt Leu att Ile 75 gtt	Gln caa Gln ggt Gly ctt Leu 60 ggt Gly	ggt Gly gaa Glu 45 aaa Lys ggt Gly tct	Lys caa Gln 30 cta Leu tca Ser acg Thr	Ala 15 ggc Gly atc Ile tta Leu tta	caa Gln tct Ser gcg Ala gaa Glu 80 act	96 144 192

RAW SEQUENCE LISTING DATE: 03/02/2007
PATENT APPLICATION: US/10/574,639
TIME: 12:58:04

Input Set : N:\efs\03_02_07\10574639_efs\seqlisting.txt

000					0.5					0.0					0.5			
299					85					90					95		, ,,	_
								aac									33	0
	Ser	GIY	Asp		Ser	GIY	Leu	Asn		Thr	Asp	GIY	Thr		ser	ser		
303				100					105					110				
								cgt									38	4
306	Ala	Phe	Tyr	Leu	Asp	Thr	Ala	Arg	Ile	Asp	Ile	Leu		His	Val	Asn		
307			115					120					125					
								tcg									43	2
310	Asp	Trp	Val	Asn	Gly	Glu	Ile	Ser	Tyr	Asp	Leu	Asn	Gly	Asp	Ser	Gly		
311		130					135					140						
313	ctt	cac	act	ggt	agc	ctt	tta	gtg	ggt	aac	ctc	aat	caa	tta	cca	gtt	48	10
314	Leu	His	Thr	Gly	Ser	Leu	Leu	Val	Gly	Asn	Leu	Asn	Gln	Leu	Pro	Val		
315	145					150					155					160		
317	tat	ggt	caa	atc	ggt	aaa	ttc	tac	cca	gat	gca	ggt	ttg	ttt	gaa	tta	52	8:
318	Tyr	Gly	Gln	Ile	Gly	Lys	Phe	Tyr	Pro	Asp	Ala	Gly	Leu	Phe	Glu	Leu		
319	•	-			165	-		-		170		_			175			
321	qct	aqt	qat	qat	qtt	tat	tct	tct	aqc	tta	gtc	aag	cgt	tat	ttc	cgt	· 57	16
	_	_	_	-	-			Ser			_	_	_					
323			•	180		•			185			•	Ū	190		_		
	cca	gat	aca	caa	aat	aat	qca	tct	qta	qqc	ttc	tat	aaa	qca	qqc	tta	62	4
								Ser										
327	-	-	195			-		200		-		•	205		-			
	cat	act		tta	act	gca	ttt	aaa	acq	tct	act	cca	caa	act	aat	act	67	12
								Lys										
331		210					215	-1-				220	-					
	act		tat	aac	caa	gca		agt	gat.	t.aa	tet		caa	aca	gat	tac	72	20
	_					_		Ser	_			_		-				
	225		-1-		· · · · ·	230					235					240		
		+++	aat	gca	aat		ata	aat	acc	act		aat.	gca	aat.	tac		76	8
								Asn										-
339			11011		245					250		0- 1		U -1	255			
	tet	aat	ato	ata		acc	aat	gac	age		act	gca	aca	aat		gga	81	6
								Asp									-	. •
343	DCI	ADII	1100	260	21011	****	11011	1100	265					270		0-1		
	act	aat	202		222	aat	caa	cta		ato	act	aat	ata	-	act	aad	86	:4
						_		Leu	_	_	_		_					-
347	1111	Gry	275	GIII	цуз	чор	nr 9	280	110	NCC	AIU	71011	285	501	111u	 ,5		
	a++	~~~		aat.	002	+++	~~~	gcc	att	act	act	tat		caa	aca	tta	91	2
								Ala									21	. 4
	116	_	Pne	Gry	PIO	FIIE	295	нта	пеп	Ата	1111	300	Ата	GIII	1111	пец		
351		290		~~~		- at		~~+	~~+		200		++~	222		+++	96	: ^
								ggt									90	, 0
	-	GIY	ьeu	Ата	ASI		Thr	Gly	GIY	THE		ьys	ьeu	ьуѕ	Ald	320		
	305				4-	310					315						100	٠.
								ttc									100	10
	Asp	ьeu	Glu	GIY		Tyr	HIS	Phe	GIn		vaı	ьуѕ	Pro	мет		vaı		
359					325					330					335			
								tat									105	,6
	Met	Leu	Gly	_	Ser	Arg	Thr	Tyr	_	Phe	Asp	Lys	Val	_	Pro	Val		
363				340					345					350				

VERIFICATION SUMMARYDATE: 03/02/2007PATENT APPLICATION: US/10/574,639TIME: 12:58:05

Input Set : N:\efs\03_02_07\10574639_efs\seqlisting.txt
Output Set: N:\CRF4\03022007\J574639.raw

```
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:496 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:501 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:506 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:511 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:516 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:521 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:526 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:532 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:537 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:542 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:5547 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:555 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:557 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:557 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:558 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
```